

## The university campus microbiome: ecological drivers of skin–gut–environment microbial interactions

**Giulia Ghisleni**<sup>1</sup>, Alice Armanni<sup>1</sup>, Sara Fumagalli<sup>1</sup>, Jessica Zampolli<sup>1</sup>, Patrizia Di Gennaro<sup>1\*</sup>,  
Antonia Bruno<sup>1\*</sup>

*E-mail:* [giulia.ghisleni@unimib.it](mailto:giulia.ghisleni@unimib.it)

<sup>1</sup> Department of Biotechnology and Biosciences, University of Milano-Bicocca

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### Abstract:

Urbanization is rapidly reshaping human habitats, with built environments (BEs) becoming the primary spaces where people live, study, and work. These settings act as ecological filters that shape both environmental and human-associated microbiomes, therefore influencing human and environmental health. However, the interactions between human (skin and gut) microbiota and the microbial communities of specific BEs, such as university campuses (unique, high-densed, and understudied) remain poorly characterized.

Here, we investigated the microbiomes of the University of Milano-Bicocca (Milan, Italy) by integrating skin and gut profiles from campus-attending students with microbial communities sampled from indoor and outdoor environments across two seasons. Using 16S rRNA gene sequencing, we assessed diversity patterns, community composition, source–sink relationships, and co-occurrence networks to explore ecological drivers of human–environment microbial connectivity.

Environmental microbiomes exhibited spatially structured and surface-specific patterns, with indoor surfaces dominated by human-associated taxa and outdoor sites reflecting greater environmental input. Human microbiomes were shaped by a combination of intrinsic and lifestyle factors, including gender, hormonal therapies, diet, cosmetic use, allergies, pet ownership, and sports activity. Environmental context (season and anthropization level of students' residence) contributed significantly to inter-individual variability. Source-tracking and network analyses revealed microbial exchange across campus spaces and between humans and their surroundings, though with compartment-specific and settings-dependent magnitude.

Collectively, this study provides the first integrated characterization of skin, gut, and built-environment microbiomes within an urban university campus. Our findings highlight how lifestyle, urban exposure, and BE features jointly modulate human-associated microbial diversity, emphasizing the value of microbiome profiling as a tool to evaluate the selective pressures of modern living spaces and to inform healthier urban design.